AMENDMENTS TO THE CLAIMS

Please amend the claims as follows:

Please cancel Claims 1-129, *i.e.*, all of the pending claims, and please add the following new claims:

1.-129. (Cancelled)

130. (New) A method for evaluating the viral fitness of a human immunodeficiency virus (HIV) comprising:

(a) culturing a cell that comprises an viral segment from the HIV and an indicator gene, wherein expression of the indicator gene depends on the activity of a gene or functional viral sequence encoded by the viral segment;

(b) measuring the activity of the indicator gene in the cell in the absence of any antiretroviral drug; and

(c) comparing the measurement of the indicator gene activity from step (b) with an activity of the indicator gene measured when steps (a) and (b) are carried out for with a reference viral segment from a reference HIV in the absence of any antiretroviral drug; wherein a difference in the indicator gene activity measured in step (b) as compared to step (c) indicates a difference in viral fitness of the HIV relative to the reference HIV.

131. (New) The method of claim 130, wherein the reference viral segment is a standard laboratory viral segment.

132. (New) The method of claim 130, wherein the reference viral segment is obtained from a treatment-naïve patient.

133. (New) The method of claim 130, wherein the cell comprises a test vector that comprises the viral segment and the indicator gene.

134. (New) The method of claim 131, wherein the test vector comprises DNA of a genomic viral vector.

135. (New) The method of claim 131, wherein the test vector comprises DNA of a subgenomic viral vector.

136. (New) The method of claim 131, wherein the test vector is introduced into the cell by infecting the cell with viral particles that comprise the test vector.

137. (New) The method of claim 130, wherein the viral segment comprises a functional viral sequence.

138. (New) The method of claim 130, wherein the viral segment is a patient-derived segment.

139. (New) The method of claim 130, wherein the viral segment comprises an HIV gene.

140. (New) The method of claim 139, wherein the HIV gene encodes HIV reverse transcriptase.

141. (New) The method of claim 139, wherein the HIV gene encodes HIV protease.

142. (New) The method of claim 139, wherein the HIV gene encodes HIV integrase.

143. (New) The method of claim 139, wherein the HIV gene is *gag*.

144. (New) The method of claim 139, wherein the HIV gene is *pol*.

145. (New) The method of claim 130, wherein the indicator gene is luciferase.

146. (New) The method of claim 130, wherein the indicator gene is lacZ.

147. (New) The method of claim 130, wherein the cell is a human cell.

148. (New) The method of claim 130, wherein the cell is from a human T cell leukemia cell line.

149. (New) The method of claim 130, wherein the cell is a Jurkat cell.

150. (New) The method of claim 130, wherein the cell is an H9 cell.

151. (New) The method of claim 130, wherein the cell is a CEM cell.

152. (New) The method of claim 130, wherein the viral fitness of the HIV is increased relative to the reference HIV.

153. (New) The method of claim 130, wherein the viral fitness of the HIV is decreased relative to the reference HIV.

154. (New) The method of claim 130, wherein the viral segment comprises nucleic acid encoding HIV integrase having a mutation at codon 66.

155. (New) The method of claim 130, wherein the viral segment comprises nucleic acid encoding HIV integrase having a mutation at codon 154.

156. (New) The method of claim 154, wherein the viral segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 153.

157. (New) The method of claim 154, wherein the viral segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 154.

158. (New) The method of claim 130, wherein the viral segment comprises nucleic acid encoding HIV reverse transcriptase having a mutation at codon 190.

159. (New) The method of claim 158, wherein the mutation at codon 190 encodes alanine (A), serine (S), cysteine (C), glutamin acid (E), valine (V), threonine (T), or glutamine (Q).

160. (New) The method of claim 130, wherein the viral segment comprises nucleic acid encoding HIV protease having a mutation at codon 25, codon 30, codon 63, codon 90, codons 30 and 63, codons 30 and 71, codons 63 and 71, or codons 30, 71, and 88.

161. (New) The method of claim 160, wherein the mutation at codon 25 encodes glycine (G), the mutations at codon 30 encode asparagine (N), the mutations at codon 63 encode proline (P), the mutations at codon 71 encode threonine (T), the mutation at codon 88 encodes aspartic acid (D), and the mutation at codon 90 encodes methionine (M).

162. (New) A method for determining the viral fitness of an HIV comprising:

(a) culturing a host cell that comprises a test vector comprising a viral segment from the HIV and an indicator gene, wherein expression of the indicator gene depends on the activity of a gene or functional viral sequence encoded by the viral segment, wherein the host cell produces viral particles that comprise the test vector;

(b) infecting a target cell with the viral particles;

(c) measuring activity of the indicator gene in the target cell;

(d) comparing the activity of the indicator gene measured in (c) with an activity of the indicator gene measured when steps (a) through (c) are carried out using a reference test vector, wherein the comparison between the activity of the indicator gene measured in step (c) relative to the activity of the indicator gene measured in (d) indicates the viral fitness of the HIV.

163. (New) The method of claim 162, further comprising the step of: (f) normalizing the activity of the indicator gene measured in step (c) by measuring an amount of viral particles used to infect the target cell in step (b).

164. (New) The method of claim 162, wherein the reference test vector comprises a standard laboratory viral segment.

165. (New) The method of claim 162, wherein the reference test vector comprises a patient-derived segment obtained from a treatment-naïve patient.

166. (New) The method of claim 162, wherein the test vector comprises DNA of a genomic viral vector.

167. (New) The method of claim 162, wherein the test vector comprises DNA of a subgenomic viral vector.

168. (New) The method of claim 162, wherein the viral segment comprises a functional viral sequence.

169. (New) The method of claim 162, wherein the viral segment is a patient-derived segment.

170. (New) The method of claim 162, wherein the viral segment comprises an HIV gene.

171. (New) The method of claim 170, wherein the HIV gene encodes HIV reverse transcriptase.

172. (New) The method of claim 170, wherein the HIV gene encodes HIV protease.

173. (New) The method of claim 170, wherein the HIV gene encodes HIV integrase.

174. (New) The method of claim 170, wherein the HIV gene is *gag*.

175. (New) The method of claim 170, wherein the HIV gene is *pol*.

176. (New) The method of claim 162, wherein the indicator gene is luciferase.

177. (New) The method of claim 162, wherein the indicator gene is lacZ.

178. (New) The method of claim 162, wherein the target cell is a human cell.

179. (New) The method of claim 162, wherein the target cell is from a human T cell leukemia cell line.

180. (New) The method of claim 162, wherein the target cell is a Jurkat cell.

181. (New) The method of claim 162, wherein the target cell is an H9 cell.

182. (New) The method of claim 162, wherein the target cell is a CEM cell.

183. (New) The method of claim 162, wherein the viral fitness of the HIV is increased relative to the reference.

184. (New) The method of claim 162, wherein the viral fitness of the HIV is decreased relative to the reference.

185. (New) The method of claim 162, wherein the viral segment comprises nucleic acid encoding HIV integrase having a mutation at codon 66.

186. (New) The method of claim 162, wherein the viral segment comprises nucleic acid encoding HIV integrase having a mutation at codon 154.

187. (New) The method of claim 185, wherein the viral segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 153.

188. (New) The method of claim 185, wherein the viral segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 154.

189. (New) The method of claim 162, wherein the viral segment comprises nucleic acid encoding HIV reverse transcriptase having a mutation at codon 190.

190. (New) The method of claim 189, wherein the mutation at codon 190 encodes alanine (A), serine (S), cysteine (C), glutamin acid (E), valine (V), threonine (T), or glutamine (Q).

191. (New) The method of claim 162, wherein the viral segment comprises nucleic acid encoding HIV protease having a mutation at codon 25, codon 30, codon 63, codon 90, codons 30 and 63, codons 30 and 71, codons 63 and 71, or codons 30, 71, and 88.

192. (New) The method of claim 191, wherein the mutation at codon 25 encodes glycine (G), the mutations at codon 30 encode asparagine (N), the mutations at codon 63 encode proline (P), the mutations at codon 71 encode threonine (T), the mutation at codon 88 encodes aspartic acid (D), and the mutation at codon 90 encodes methionine (M).